



SEQUENCE LISTING

<110> Duvick, Jonathan P.
Gilliam, Jacob T.
Maddox, Joyce R.
Crasta, Oswald R.
Folkerts, Otto

<120> Amino Polyol Amine Oxidase
Polynucleotides and Related Polypeptides and Methods of Use

<130> 0875C

<150> US 60/092,936

<151> 1998-07-15

<150> US 09/352,168

<151> 1999-07-12

<160> 33

<170> FastSEQ for Windows Version 3.0

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<212> DNA

<213> *Exophiala spinifera*.

<220>

<221> misc_feature

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attgtcgatc gacgtcgatg ctggtatctc tggcaaata gatgggggtca cagctcgatt	180
ggaggacgcc cgagaagcct tggtcgcgcc accacggctt gtcccatagc aagactatct	240
tgctatagta gccacaggata gaattttccg ccaatgcttg cttctcggcg ggaagaggtg	300
gtgaaaatgt caaggtggga tacaaggttg tcggtaacga aaccancacc tttttgcttc	360
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tacaaggttg tcggtaacga aaccaccacc tttttgcttc ggaacacggc gcccgaggcc	120
gacgtactg tacagccgga tgccgactgc tcaatttcag cgacgggggt gttgaggtgc	180
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<213> Artificial Sequence

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 tgggtttcggtt accgacaacc ttgtatccc 29

<210> 4
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 gagttggtcc cagacagact tttgtcgt 28

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gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt	96
Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu	
20 25 30	
gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tgc ggt	144
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly	
35 40 45	
ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac	192
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp	
50 55 60	
agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag	240
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu	
65 70 75 80	
ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac	288
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp	
85 90 95	
ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag	336
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu	
100 105 110	
gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc	384
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile	
115 120 125	
gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg	432
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg	
130 135 140	

ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu 145 150 155 160	480
cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly 165 170 175	528
gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys 180 185 190	576
agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly 195 200 205	624
cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met 210 215 220	672
tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala 225 230 235 240	720
gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly 245 250 255	768
gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu 260 265 270	816
tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala 275 280 285	864
ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val 290 295 300	912
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tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val 325 330 335	1008
gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg 340 345 350	1056
aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp 355 360 365	1104
caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro 370 375 380	1152
gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly 1200	1200

385		390		395		400	
gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg							1248
Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser							
	405			410		415	
gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg							1296
Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr							
	420			425		430	
tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa							1344
Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln							
	435			440		445	
cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca							1386
Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala							
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tag							1389

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 <212> PRT
 <213> *Exophiala spinifera*

<400> 6

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			20					25					30		
Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly
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Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp
	50					55					60				
Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu
65					70					75					80
Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp
			85					90						95	
Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu
			100					105						110	
Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile
		115					120					125			
Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg
		130				135					140				
Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu
145					150					155					160
Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly
				165				170						175	
Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys
			180					185					190		
Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly
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Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met
		210				215					220				
Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala
225					230					235					240
Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly
				245				250						255	
Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu
			260					265					270		
Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala
		275					280					285			

Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val
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Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln
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Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val
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Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg
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Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp
		355					360					365			
Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro
	370					375					380				
Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly
385					390					395					400
Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser
				405					410					415	
Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr
			420					425					430		
Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln
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gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt															96	
Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	
			20					25					30			
gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt															144	
Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	
		35					40					45				
ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac															192	
Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	
		50				55						60				
agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag															240	
Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	
	65					70				75				80		
ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac															288	
Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	
				85					90					95		

ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag	336
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu	
100 105 110	
ggt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc	384
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile	
115 120 125	
gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg	432
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg	
130 135 140	
ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg	480
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu	
145 150 155 160	
cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt	528
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly	
165 170 175	
gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag	576
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys	
180 185 190	
agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg	624
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly	
195 200 205	
cag tat gtg cga tgc aaa aca g gtgcgtgtgg tgctgtctca ggtgggggac	676
Gln Tyr Val Arg Cys Lys Thr	
210 215	
tcgtttctca gtggtcattc cag gt atg cag tcg att tgc cat gcc atg tca	728
Gly Met Gln Ser Ile Cys His Ala Met Ser	
220 225	
aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa	776
Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu	
230 235 240	
att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc	824
Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala	
245 250 255	
gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat	872
Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr	
260 265 270	
ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg	920
Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu	
275 280 285	
gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg	968
Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp	
290 295 300 305	
gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg	1016
Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser	
310 315 320	
agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat	1064

Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp		
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cga	caa	tgg	tcc	att	acc	tgt	ttc	atg	gtc	gga	gac	ccg	gga	cgg	aag		1112
Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys		
		340					345					350					
tgg	tcc	caa	cag	tcc	aag	cag	gta	cga	caa	aag	tct	gtc	tgg	gac	caa		1160
Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln		
	355					360					365						
ctc	cgc	gca	gcc	tac	gag	aac	gcc	ggg	gcc	caa	gtc	cca	gag	ccg	gcc		1208
Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala		
370					375				380						385		
aac	gtg	ctc	gaa	atc	gag	tgg	tcg	aag	cag	cag	tat	ttc	caa	gga	gct		1256
Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala		
				390					395					400			
ccg	agc	gcc	gtc	tat	ggg	ctg	aac	gat	ctc	atc	aca	ctg	ggt	tcg	gcg		1304
Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala		
			405					410					415				
ctc	aga	acg	ccg	ttc	aag	agt	gtt	cat	ttc	gtt	gga	acg	gag	acg	tct		1352
Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser		
		420					425					430					
tta	gtt	tgg	aaa	ggg	tat	atg	gaa	ggg	gcc	ata	cga	tcg	ggt	caa	cga		1400
Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg		
	435					440					445						
ggt	gct	gca	gaa	gtt	gtg	gct	agc	ctg	gtg	cca	gca	gca	tag				1442
Gly	Ala	Ala	Glu	Val	Ala	Ala	Ser	Leu	Val	Pro	Ala	Ala					
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<210> 8
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 <213> Exophiala spinifera

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Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	
	35					40						45				
Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	
	50				55						60					
Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	
65				70						75				80		
Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	
			85				90							95		
Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	
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Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	
	115					120					125					
Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	
	130				135						140					
Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	
145					150					155					160	

Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly
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Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys
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Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly
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Gln	Tyr	Val	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met
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Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala
225					230					235					240
Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly
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Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu
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Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala
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Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val
	290					295					300				
Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln
305					310					315					320
Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val
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Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg
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Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp
		355					360					365			
Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro
	370					375					380				
Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly
385					390					395					400
Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser
			405						410					415	
Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr
			420					425					430		
Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln
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Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala		
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<211> 458

<212> PRT

<213> Exophiala spinifera

<400> 9

Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu
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Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu
			20					25					30		
Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly
		35					40					45			
Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp
	50					55					60				
Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu
65					70					75					80
Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp
				85					90					95	
Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu
			100					105					110		
Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	
		115					120				125				
Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg

130		135		140	
Leu Asp Ser Val Ser Phe	Ala His Tyr Cys Glu Lys Glu Leu Asn Leu				
145	150	155	160		
Pro Ala Val Leu Gly Val	Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly				
	165	170	175		
Val Glu Ala His Glu Ile	Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys				
	180	185	190		
Ser Ala Thr Gly Leu Ser	Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly				
	195	200	205		
Gln Tyr Val Arg Cys Lys	Thr Gly Ala Cys Gly Val Val Ser Gly Gly				
	210	215	220		
Gly Leu Val Ser Gln Trp	Ser Phe Gln Val Cys Ser Arg Phe Ala Met				
225	230	235	240		
Pro Cys Gln Arg Asn Leu	Phe Gln Ala Gln Cys Thr Ser Thr Pro Pro				
	245	250	255		
Ser Leu Lys Leu Ser Ser	Arg His Pro Ala Val Gln Tyr Asp Arg Pro				
	260	265	270		
Arg Ala Pro Cys Ser Glu	Ala Lys Arg Trp Trp Phe Arg Tyr Arg Gln				
	275	280	285		
Pro Cys Ile Pro Pro His	Phe His His Leu Phe Pro Pro Arg Ser Lys				
	290	295	300		
His Trp Arg Lys Ile Leu	Ser Trp Ala Thr Ile Ala Arg Ser Ser Tyr				
305	310	315	320		
Gly Thr Ser Arg Gly Gly	Ala Asn Lys Ala Ser Arg Ala Ser Ser Asn				
	325	330	335		
Arg Ala Val Thr Pro Ser	His Leu Pro Glu Ile Pro Ala Ser Thr Ser				
	340	345	350		
Ile Asp Asn Gly Pro Leu	Pro Val Ser Trp Ser Glu Thr Arg Asp Gly				
	355	360	365		
Ser Gly Pro Asn Ser Pro	Ser Arg Tyr Asp Lys Ser Leu Ser Gly Thr				
	370	375	380		
Asn Ser Ala Gln Pro Thr	Arg Thr Pro Gly Pro Lys Ser Gln Ser Arg				
385	390	395	400		
Pro Thr Cys Ser Lys Ser	Ser Gly Arg Ser Ser Ile Ser Lys Glu				
	405	410	415		
Leu Arg Ala Pro Ser Met	Gly Thr Ile Ser Ser His Trp Val Arg Arg				
	420	425	430		
Ser Glu Arg Arg Ser Arg	Val Phe Ile Ser Leu Glu Arg Arg Arg Leu				
	435	440	445		
Phe Gly Lys Gly Ile Trp	Lys Gly Pro Tyr				
450	455				

<210> 10
 <211> 1392
 <212> DNA
 <213> *Exophiala spinifera*

 <220>
 <221> CDS
 <222> (1)...(1389)

 <221> misc_feature
 <222> (1)...(3)
 <223> Extra lysine in K:trAPAO

<400> 10		
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt		48
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly		
1 5 10 15		
ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt		96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val		

20										25										30										
ctt	gag	gcg	atg	gat	cgt	gta	ggg	gga	aag	act	ctg	agc	gta	caa	tcg		144													
Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser															
		35					40					45																		
ggc	ccc	ggc	agg	acg	act	atc	aac	gac	ctc	ggc	gct	gcg	tgg	atc	aat		192													
Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn															
	50					55				60																				
gac	agc	aac	caa	agc	gaa	gta	tcc	aga	ttg	ttt	gaa	aga	ttt	cat	ttg		240													
Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu															
	65				70				75						80															
gag	ggc	gag	ctc	cag	agg	acg	act	gga	aat	tca	atc	cat	caa	gca	caa		288													
Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln															
			85					90					95																	
gac	ggc	aca	acc	act	aca	gct	cct	tat	ggc	gac	tcc	ttg	ctg	agc	gag		336													
Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu															
		100					105					110																		
gag	gtt	gca	agt	gca	ctt	gcg	gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg		384													
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu															
		115				120					125																			
atc	gaa	gag	cat	agc	ctt	caa	gac	ctc	aag	gcg	agc	cct	cag	gcg	aag		432													
Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys															
	130					135					140																			
cgg	ctc	gac	agt	gtg	agc	ttc	gcg	cac	tac	tgt	gag	aag	gaa	cta	aac		480													
Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn															
	145				150					155					160															
ttg	cct	gct	gtt	ctc	ggc	gta	gca	aac	cag	atc	aca	cgc	gct	ctg	ctc		528													
Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu															
			165						170					175																
ggc	gtg	gaa	gcc	cac	gag	atc	agc	atg	ctt	ttt	ctc	acc	gac	tac	atc		576													
Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile															
			180				185						190																	
aag	agt	gcc	acc	ggc	ctc	agt	aat	att	ttc	tcg	gac	aag	aaa	gac	ggc		624													
Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly															
		195					200					205																		
ggg	cag	tat	atg	cga	tgc	aaa	aca	ggc	atg	cag	tcg	att	tgc	cat	gcc		672													
Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala															
	210					215					220																			
atg	tca	aag	gaa	ctt	gtt	cca	ggc	tca	gtg	cac	ctc	aac	acc	ccc	gtc		720													
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val															
	225				230				235						240															
gct	gaa	att	gag	cag	tcg	gca	tcc	ggc	tgt	aca	gta	cga	tcg	gcc	tcg		768													
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser															
			245					250						255																
ggc	gcc	gtg	ttc	cga	agc	aaa	aag	gtg	gtg	gtt	tcg	tta	ccg	aca	acc		816													
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr															
		260						265					270																	

ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	
275 280 285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc	912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
290 295 300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc	960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu	
305 310 315 320	
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac	1008
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp	
325 330 335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga	1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	
340 345 350	
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg	1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp	
355 360 365	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag	1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu	
370 375 380	
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa	1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln	
385 390 395 400	
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt	1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly	
405 410 415	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag	1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu	
420 425 430	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt	1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly	
435 440 445	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca	1389
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala	
450 455 460	

tag 1392

<210> 11
 <211> 463
 <212> PRT
 <213> Exophiala spinifera

<220>
 <223> Extra lysine in the polypeptide sequence of
 K:trAPAO, 463 aa.

<400> 11
 Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
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Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val
			20					25					30		
Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser
		35					40				45				
Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn
	50					55				60					
Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu
65					70					75					80
Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln
				85				90						95	
Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu
			100					105					110		
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu
		115					120					125			
Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys
	130					135						140			
Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn
145					150					155					160
Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu
			165					170						175	
Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile
			180					185					190		
Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly
		195					200					205			
Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala
	210					215				220					
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val
225					230					235					240
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser
			245					250						255	
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr
		260						265					270		
Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln
		275					280					285			
Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe
	290					295					300				
Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu
305					310					315					320
Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp
			325					330						335	
Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly
		340						345					350		
Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp
		355					360					365			
Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu
	370					375					380				
Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln
385					390					395					400
Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly
			405					410						415	
Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu
			420					425					430		
Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly
		435				440						445			
Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala	
	450					455					460				

<210> 12

<211> 34

<212> DNA

<213> Artificial Sequence

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<220>
<223> Primer sequence designed for cloning DNA into
        expression vectors, N23256

<400> 12
ggggaattca aagacaacgt tgcggacgtg gtag
34

<210> 13
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer sequence designed for cloning DNA into
        expression vectors, N23259

<400> 13
ggggcggcgc cctatgctgc tggcaccagg ctag
34

<210> 14
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide for 3' RACE, N21965

<400> 14
tggtttcggt accgacaacc ttgtatccc
29

<210> 15
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide for 5' race, N21968

<400> 15
gagtttgtcc cagacagact tttgtcgt
28

<210> 16
<211> 1673
<212> DNA
<213> Exophiala spinifera

<220>
<221> sig_peptide
<222> (1)...(267)
<223> yeast alpha mating factor secretion signal.

<221> CDS
<222> (1)...(1662)

<400> 16
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Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
-85 -80 -75
48

gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa
Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
-70 -65 -60
96

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att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc	144
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe	
-55 -50 -45	
gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg	192
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu	
-40 -35 -30	
ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta	240
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val	
-25 -20 -15 -10	
tct ctc gag aaa aga gag gct gaa gct gaa ttc aaa gac aac gtt gcg	288
Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala	
-5 1 5	
gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc	336
Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg	
10 15 20	
aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat	384
Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp	
25 30 35	
cgt gta ggg gga aag act ctg agc gta caa tgc ggt ccc ggc agg acg	432
Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr	
40 45 50 55	
act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc	480
Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser	
60 65 70	
gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag	528
Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln	
75 80 85	
agg acg act gga aat tca atc cat caa gca caa gac ggt aca acc act	576
Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr	
90 95 100	
aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca	624
Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala	
105 110 115	
ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc	672
Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser	
120 125 130 135	
ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg	720
Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val	
140 145 150	
agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc	768
Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu	
155 160 165	
ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac	816
Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His	
170 175 180	
gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt	864

Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly		
185						190					195						
ctc	agt	aat	att	ttc	tcg	gac	aag	aaa	gac	ggc	ggg	cag	tat	atg	cga	912	
Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg		
200					205					210					215		
tgc	aaa	aca	ggg	atg	cag	tcg	att	tgc	cat	gcc	atg	tca	aag	gaa	ctt	960	
Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu		
				220					225					230			
gtt	cca	ggc	tca	gtg	cac	ctc	aac	acc	ccc	gtc	gct	gaa	att	gag	cag	1008	
Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln		
			235					240					245				
tcg	gca	tcc	ggc	tgt	aca	gta	cga	tcg	gcc	tcg	ggc	gcc	gtg	ttc	cga	1056	
Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg		
		250					255					260					
agc	aaa	aag	gtg	gtg	gtt	tcg	tta	ccg	aca	acc	ttg	tat	ccc	acc	ttg	1104	
Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu		
	265					270					275						
aca	ttt	tca	cca	cct	ctt	ccc	gcc	gag	aag	caa	gca	ttg	gcg	gaa	aat	1152	
Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn		
280					285					290					295		
tct	atc	ctg	ggc	tac	tat	agc	aag	ata	gtc	ttc	gta	tgg	gac	aag	ccg	1200	
Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro		
				300					305					310			
tgg	tgg	cgc	gaa	caa	ggc	ttc	tcg	ggc	gtc	ctc	caa	tcg	agc	tgt	gac	1248	
Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp		
			315					320					325				
ccc	atc	tca	ttt	gcc	aga	gat	acc	agc	atc	gac	gtc	gat	cga	caa	tgg	1296	
Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp		
		330					335					340					
tcc	att	acc	tgt	ttc	atg	gtc	gga	gac	ccg	gga	cgg	aag	tgg	tcc	caa	1344	
Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln		
	345					350					355						
cag	tcc	aag	cag	gta	cga	caa	aag	tct	gtc	tgg	gac	caa	ctc	cgc	gca	1392	
Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala		
360					365					370					375		
gcc	tac	gag	aac	gcc	ggg	gcc	caa	gtc	cca	gag	ccg	gcc	aac	gtg	ctc	1440	
Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu		
				380					385					390			
gaa	atc	gag	tgg	tcg	aag	cag	cag	tat	ttc	caa	gga	gct	ccg	agc	gcc	1488	
Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala		
			395					400					405				
gtc	tat	ggg	ctg	aac	gat	ctc	atc	aca	ctg	ggg	tcg	gcg	ctc	aga	acg	1536	
Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr		
		410					415					420					
ccg	ttc	aag	agt	gtt	cat	ttc	gtt	gga	acg	gag	acg	tct	tta	gtt	tgg	1584	
Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp		
	425					430					435						

aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca 1632
 Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala
 440 445 450 455

gaa gtt gtg gct agc ctg gtg cca gca gca taggcggccg c 1673
 Glu Val Val Ala Ser Leu Val Pro Ala Ala
 460 465

<210> 17
 <211> 554
 <212> PRT
 <213> Exophiala spinifera

<220>
 <221> SIGNAL
 <222> (1)...(89)
 <223> yeast alpha mating factor secretion signal.

<400> 17
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 Ala Leu Ala Ala Pro Val Asn Thr Thr Glu Asp Glu Thr Ala Gln
 -70 -65 -60
 Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
 -55 -50 -45
 Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
 -40 -35 -30
 Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
 -25 -20 -15 -10
 Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala
 -5 1 5
 Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg
 10 15 20
 Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp
 25 30 35
 Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr
 40 45 50 55
 Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser
 60 65 70
 Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln
 75 80 85
 Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr
 90 95 100
 Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala
 105 110 115
 Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser
 120 125 130 135
 Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val
 140 145 150
 Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu
 155 160 165
 Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His
 170 175 180
 Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly
 185 190 195
 Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg
 200 205 210 215
 Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu
 220 225 230
 Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln

Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu		
			20					25					30				
tat	gag	cgc	gat	gaa	ggt	gat	aaa	tgg	cga	aac	aaa	aag	ttt	gaa	ttg		144
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu		
		35					40					45					
ggt	ttg	gag	ttt	ccc	aat	ctt	cct	tat	tat	att	gat	ggt	gat	ggt	aaa		192
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys		
	50					55					60						
tta	aca	cag	tct	atg	gcc	atc	ata	cgt	tat	ata	gct	gac	aag	cac	aac		240
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn		
	65				70				75						80		
atg	ttg	ggt	ggt	tgt	cca	aaa	gag	cgt	gca	gag	att	tca	atg	ctt	gaa		288
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu		
				85				90						95			
gga	gcg	ggt	ttg	gat	att	aga	tac	ggt	ggt	tcg	aga	att	gca	tat	agt		336
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser		
			100					105					110				
aaa	gac	ttt	gaa	act	ctc	aaa	ggt	gat	ttt	ctt	agc	aag	cta	cct	gaa		384
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu		
		115					120					125					
atg	ctg	aaa	atg	ttc	gaa	gat	cgt	tta	tgt	cat	aaa	aca	tat	tta	aat		432
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn		
	130					135					140						
ggt	gat	cat	gta	acc	cat	cct	gac	ttc	atg	ttg	tat	gac	gct	ctt	gat		480
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp		
	145				150					155				160			
ggt	ggt	tta	tac	atg	gac	cca	atg	tgc	ctg	gat	gcg	ttc	cca	aaa	tta		528
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu		
				165				170						175			
ggt	tgt	ttt	aaa	aaa	cgt	att	gaa	gct	atc	cca	caa	att	gat	aag	tac		576
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr		
			180					185					190				
ttg	aaa	tcc	agc	aag	tat	ata	gca	tgg	cct	ttg	cag	ggc	tgg	caa	gcc		624
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala		
		195					200					205					
acg	ttt	ggt	ggt	ggc	gac	cat	cct	cca	aaa	tcg	gat	ctg	ggt	ccg	cgt		672
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg		
	210					215					220						
gga	tcc	ccg	gaa	ttc	aaa	gac	aac	ggt	gcg	gac	gtg	gta	gtg	gtg	ggc		720
Gly	Ser	Pro	Glu	Phe	Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly		
	225				230					235					240		
gct	ggc	ttg	agc	ggt	ttg	gag	acg	gca	cgc	aaa	gtc	cag	gcc	gcc	ggt		768
Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly		
				245				250					255				
ctg	tcc	tgc	ctc	ggt	ctt	gag	gcg	atg	gat	cgt	gta	ggg	gga	aag	act		816
Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr		
			260					265					270				

ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc ggc Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly 275 280 285	864
gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg ttt Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe 290 295 300	912
gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat tca Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser 305 310 315 320	960
atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt gac Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp 325 330 335	1008
tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc ccc Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro 340 345 350	1056
gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag gcg Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala 355 360 365	1104
agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac tgt Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys 370 375 380	1152
gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag atc Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile 385 390 395 400	1200
aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt ttt Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe 405 410 415	1248
ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc tcg Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser 420 425 430	1296
gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg cag Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln 435 440 445	1344
tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg cac Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His 450 455 460	1392
ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt aca Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr 465 470 475 480	1440
gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val 485 490 495	1488
tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct ctt Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu 500 505 510	1536
ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac tat	1584

Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr		
		515					520					525					
agc	aag	ata	gtc	ttc	gta	tgg	gac	aag	ccg	tgg	tgg	cgc	gaa	caa	ggc	1632	
Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly		
	530					535				540							
ttc	tcg	ggc	gtc	ctc	caa	tcg	agc	tgt	gac	ccc	atc	tca	ttt	gcc	aga	1680	
Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg		
545					550				555						560		
gat	acc	agc	atc	gac	gtc	gat	cga	caa	tgg	tcc	att	acc	tgt	ttc	atg	1728	
Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met		
				565					570					575			
gtc	gga	gac	ccg	gga	cgg	aag	tgg	tcc	caa	cag	tcc	aag	cag	gta	cga	1776	
Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg		
			580					585					590				
caa	aag	tct	gtc	tgg	gac	caa	ctc	cgc	gca	gcc	tac	gag	aac	gcc	ggg	1824	
Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly		
	595					600						605					
gcc	caa	gtc	cca	gag	ccg	gcc	aac	gtg	ctc	gaa	atc	gag	tgg	tcg	aag	1872	
Ala	Gln	Val	Pro	Glu	Pro		Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys		
	610					615						620					
cag	cag	tat	ttc	caa	gga	gct	ccg	agc	gcc	gtc	tat	ggg	ctg	aac	gat	1920	
Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp		
625					630				635						640		
ctc	atc	aca	ctg	ggg	tcg	gcg	ctc	aga	acg	ccg	ttc	aag	agt	gtt	cat	1968	
Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His		
				645					650					655			
ttc	gtt	gga	acg	gag	acg	tct	tta	gtt	tgg	aaa	ggg	tat	atg	gaa	ggg	2016	
Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly		
			660					665					670				
gcc	ata	cga	tcg	ggg	caa	cga	ggg	gct	gca	gaa	gtt	gtg	gct	agc	ctg	2064	
Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu		
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gtg	cca	gca	gca	tag												2079	
Val	Pro	Ala	Ala														
	690																

<210> 19
 <211> 692
 <212> PRT
 <213> Unknown

<220>
 <223> GST:K:trAPAO; GST + linker, aa 1-229; K:trAPAO, aa 230-692

<400> 19
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 1 5 10 15
 Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30

Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu
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Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys
	50					55					60				
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn
65					70					75					80
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu
				85					90					95	
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser
			100					105					110		
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu
		115					120					125			
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn
	130					135					140				
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp
145					150					155					160
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu
				165					170					175	
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr
			180					185					190		
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala
		195					200					205			
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg
	210					215					220				
Gly	Ser	Pro	Glu	Phe	Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly
225					230					235					240
Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly
				245					250					255	
Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr
			260					265					270		
Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly
		275					280					285			
Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe
	290					295					300				
Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser
305					310					315					320
Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp
				325					330					335	
Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro
			340					345					350		
Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala
		355					360					365			
Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys
	370					375					380				
Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile
385					390					395					400
Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe
				405					410					415	
Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser
			420					425					430		
Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln
		435					440					445			
Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His
	450					455					460				
Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr
465					470					475					480
Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val
				485					490					495	
Ser	Leu	Pro	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	
			500					505					510		
Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr
		515					520					525			

Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly
 530 535 540
 Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg
 545 550 555 560
 Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met
 565 570 575
 Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg
 580 585 590
 Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly
 595 600 605
 Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys
 610 615 620
 Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp
 625 630 635 640
 Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His
 645 650 655
 Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly
 660 665 670
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 Val Pro Ala Ala
 690

<210> 20
 <211> 1464
 <212> DNA
 <213> Unknown

<220>
 <221> sig_peptide
 <222> (1)...(72)
 <223> Barley Alpha Amylase signal sequence.

<221> misc_feature
 <222> (73)...(1464)
 <223> K:trAPAOcDNA

<221> CDS
 <222> (1)...(1461)

<223> Nucleotide sequence of K:trAPAO translational fusion with barley alpha amylase signal sequence, for expression and secretion of the mature trAPAO in maize. Nucleotides 1-72, barley alpha amylase signal sequence, nucleotides 73-75, added lysine residue; nucleotides 76 -1464 , trAPAO cDNA.

<221> misc_feature
 <222> (73)...(75)
 <223> Added lysine residue

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 Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
 -20 -15 -10

 ctc tcc gcc tcc ctc gcc agc ggc aaa gac aac gtt gcg gac gtg gta 96
 Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val
 -5 1 5

 gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag 144
 Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln

10	15	20	
gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly 25 30 35 40			192
gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn 45 50 55			240
gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser 60 65 70			288
aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr 75 80 85			336
gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct cct Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro 90 95 100			384
tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu 105 110 115 120			432
ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp 125 130 135			480
ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala 140 145 150			528
cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala 155 160 165			576
aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser 170 175 180			624
atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn 185 190 195 200			672
att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr 205 210 215			720
ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly 220 225 230			768
tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser 235 240 245			816
ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys 250 255 260			864

gtg gtg gtt tgc tta ccg aca acc ttg tat ccc acc ttg aca ttt tca	912
Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser	
265 270 275 280	
cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg	960
Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu	
285 290 295	
ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc	1008
Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg	
300 305 310	
gaa caa ggc ttc tgc gcc gtc ctc caa tgc agc tgt gac ccc atc tca	1056
Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser	
315 320 325	
ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc	1104
Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr	
330 335 340	
tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag	1152
Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys	
345 350 355 360	
cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag	1200
Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu	
365 370 375	
aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag	1248
Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu	
380 385 390	
tgg tgc aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg	1296
Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly	
395 400 405	
ctg aac gat ctc atc aca ctg ggt tgc gcg ctc aga acg ccg ttc aag	1344
Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys	
410 415 420	
agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat	1392
Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr	
425 430 435 440	
atg gaa ggg gcc ata cga tgc ggt caa cga ggt gct gca gaa gtt gtg	1440
Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val	
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gct agc ctg gtg cca gca gca tag	1464
Ala Ser Leu Val Pro Ala Ala	
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 <212> PRT
 <213> Unknown

 <220>
 <221> SIGNAL
 <222> (1)...(24)

<223> K:trAPAO translational fusion with barley alpha
amylase signal sequence, for expression and
secretion of the mature trAPAO in maize.

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Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val
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Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln
10 15 20
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly
25 30 35 40
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn
45 50 55
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser
60 65 70
Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr
75 80 85
Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro
90 95 100
Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu
105 110 115 120
Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp
125 130 135
Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala
140 145 150
His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala
155 160 165
Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser
170 175 180
Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn
185 190 195 200
Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr
205 210 215
Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly
220 225 230
Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser
235 240 245
Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys
250 255 260
Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser
265 270 275 280
Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu
285 290 295
Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg
300 305 310
Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser
315 320 325
Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr
330 335 340
Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys
345 350 355 360
Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu
365 370 375
Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu
380 385 390
Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly
395 400 405
Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys
410 415 420
Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr

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425          430          435          440
Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val
          445          450          455
Ala Ser Leu Val Pro Ala Ala
          460

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180										185					190					
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Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val					
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tcc	aga	ttg	ttt	gaa	aga	ttt	cat	ttg	gag	ggc	gag	ctc	cag	agg	acg	672				
Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr					
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Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala					
225					230					235					240					
cct	tat	ggc	gac	tcc	ttg	ctg	agc	gag	gag	gtt	gca	agt	gca	ctt	gcg	768				
Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala					
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gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg	atc	gaa	gag	cat	agc	ctt	caa	816				
Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln					
			260				265						270							
gac	ctc	aag	gcg	agc	cct	cag	gcg	aag	cgg	ctc	gac	agt	gtg	agc	ttc	864				
Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe					
		275					280					285								
gcg	cac	tac	tgt	gag	aag	gaa	cta	aac	ttg	cct	gct	gtt	ctc	ggc	gta	912				
Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val					
	290					295				300										
gca	aac	cag	atc	aca	cgc	gct	ctg	ctc	ggc	gtg	gaa	gcc	cac	gag	atc	960				
Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile					
305					310					315					320					
agc	atg	ctt	ttt	ctc	acc	gac	tac	atc	aag	agt	gcc	acc	ggc	ctc	agt	1008				
Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser					
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aat	att	ttc	tcg	gac	aag	aaa	gac	ggc	ggg	cag	tat	atg	cga	tgc	aaa	1056				
Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys					
			340					345					350							
aca	ggc	atg	cag	tcg	att	tgc	cat	gcc	atg	tca	aag	gaa	ctt	gtt	cca	1104				
Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro					
		355					360					365								
ggc	tca	gtg	cac	ctc	aac	acc	ccc	gtc	gct	gaa	att	gag	cag	tcg	gca	1152				
Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala					
	370					375					380									
tcc	ggc	tgt	aca	gta	cga	tcg	gcc	tcg	ggc	gcc	gtg	ttc	cga	agc	aaa	1200				
Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys					
385					390					395					400					
aag	gtg	gtg	gtt	tcg	tta	ccg	aca	acc	ttg	tat	ccc	acc	ttg	aca	ttt	1248				
Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe					
				405					410					415						
tca	cca	cct	ctt	ccc	gcc	gag	aag	caa	gca	ttg	gcg	gaa	aat	tct	atc	1296				
Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile					
			420					425					430							

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Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp	
435 440 445	
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc	1392
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile	
450 455 460	
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att	1440
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile	
465 470 475 480	
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc	1488
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser	
485 490 495	
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac	1536
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr	
500 505 510	
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc	1584
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile	
515 520 525	
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat	1632
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr	
530 535 540	
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc	1680
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe	
545 550 555 560	
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg	1728
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly	
565 570 575	
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt	1776
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val	
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Val Ala Ser Leu Val Pro Ala Ala	
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 Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
 35 40 45
 Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
 50 55 60
 Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
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Val Ala Ser Leu Val Pro Ala Ala Val
595 580 585 590
600

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<212> DNA
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sequence: espl mat: an artificial spacer sequence
and K:trAPAO

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<222> (73)...(1575)
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<223> spacer sequence

<221> misc_feature
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<221> CDS
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<222> (1612)...(1614)
<223> Extra lysine

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ctc tcc gcc tcc ctc gcc agc ggc gct cct act gtc aag att gat gct 96
Leu Ser Ala Ser Leu Ala Ser Gly Ala Pro Thr Val Lys Ile Asp Ala
-5 1 5
ggg atg gtg gtc ggc acg act act act gtc ccc ggc acc act gcg acc 144
Gly Met Val Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr
10 15 20
gtc agc gag ttc ttg ggc gtt cct ttt gcc gcc tct ccg aca cga ttt 192
Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe
25 30 35 40
gcg cct cct act cgt ccc gtg cct tgg tca acg cct ttg caa gcc act 240
Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr
45 50 55
gca tat ggt cca gca tgc cct caa caa ttc aat tac ccc gaa gaa ctc 288
Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu
60 65 70

cgt gag att acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt	336
Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly	
75 80 85	
gaa agt gag gac tgc ctg aac ctc aac atc tac gtc cca gga act gag	384
Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu	
90 95 100	
aac aca aac aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa	432
Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu	
105 110 115 120	
tat ggt tgg aat tca ttc cac ctt tac gac ggg gct agt ttc gca gcc	480
Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala	
125 130 135	
aat cag gat gtc atc gcc gtg acc atc aac tac aga acg aac att ctg	528
Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu	
140 145 150	
ggg ttc cct gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg	576
Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly	
155 160 165	
ttc cta gac caa agg ttt gct ttg gat tgg gta cag cgg aac atc gca	624
Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala	
170 175 180	
gcc ttt ggc ggt gat cct cga aag gtc aca ata ttt ggg cag agt gcg	672
Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala	
185 190 195 200	
ggg ggc aga agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca	720
Gly Gly Arg Ser Val Asp Val Leu Leu Ser Thr Ser Met Pro His Asn Pro	
205 210 215	
ccc ttc cga gca gca atc atg gag tcc ggt gtg gct aac tac aac ttc	768
Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe	
220 225 230	
ccc aag gga gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc	816
Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu	
235 240 245	
aac tgt acc acc agt atc gac atc ttg agt tgt atg aga aga gtc gat	864
Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp	
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Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu	
265 270 275 280	
tac acg ttg gac aac gta acg gct gtg tac cgt tct gaa acg gct cgc	960
Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg	
285 290 295	
acg act ggt gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc	1008
Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala	
300 305 310	
aac gac gga ctt ctc ttt gtc ctc ggg gag aat gac acc caa gca tat	1056
Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr	

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att gcc gcc att gag acc gag gta aga ttc cag tgt cct tct gcc atc Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile 365 370 375			1200
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tac aat gcg acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val 395 400 405			1296
tac cac agc tct gaa gtc ggg atg gtg ttt ggc acg tat cct gtc gca Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala 410 415 420			1344
agt gcg acc gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala 425 430 435 440			1392
tgg gcg gcc ttt gcc aaa aac ccc atg aat ggg cct ggg tgg aaa caa Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln 445 450 455			1440
gtg ccg aat gtc gcg gcg ctt ggc tca cca ggc aaa gcc atc cag gtt Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val 460 465 470			1488
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agc ggc gga ggc agc ggc gga ggc agc aaa gac aac gtt gcg gac gtg Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val 505 510 515 520			1632
gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val 525 530 535			1680
cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val 540 545 550			1728
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cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala 620 625 630	1968
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln 635 640 645	2016
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 650 655 660	2064
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 665 670 675 680	2112
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 685 690 695	2160
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser 700 705 710	2208
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys 715 720 725	2256
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro 730 735 740	2304
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala 745 750 755 760	2352
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys 765 770 775	2400
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe 780 785 790	2448
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile 795 800 805	2496
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp	2544

810	815	820	
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc			2592
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile			
825	830	835	840
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att			2640
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile			
	845	850	855
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc			2688
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser			
	860	865	870
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac			2736
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr			
	875	880	885
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc			2784
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile			
	890	895	900
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat			2832
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr			
	905	910	915
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc			2880
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe			
	925	930	935
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg			2928
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly			
	940	945	950
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt			2976
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val			
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gtg gct agc ctg gtg cca gca gca tag			3003
Val Ala Ser Leu Val Pro Ala Ala			
	970	975	

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 <212> PRT
 <213> Unknown

<220>
 <221> SIGNAL
 <222> (1)...(24)

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 -5 1 5
 Gly Met Val Val Gly Thr Thr Thr Val Pro Gly Thr Thr Ala Thr
 10 15 20
 Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe
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 Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr

				45					50					55	
Ala	Tyr	Gly	Pro	60	Ala	Cys	Pro	Gln	Gln	Phe	Asn	Tyr	Pro	Glu	Glu
Arg	Glu	Ile	Thr	75	Met	Ala	Trp	Phe	Asn	Thr	Pro	Pro	Pro	Ser	Ala
Glu	Ser	Glu	Asp	90	Cys	Leu	Asn	Leu	Asn	Ile	Tyr	Val	Pro	Gly	Thr
Asn	Thr	Asn	Lys	105	Ala	Val	Met	Val	Trp	Ile	Tyr	Gly	Gly	Ala	Leu
Tyr	Gly	Trp	Asn	120	Ser	Phe	His	Leu	Tyr	Asp	Gly	Ala	Ser	Phe	Ala
Asn	Gln	Asp	Val	135	Ile	Ala	Val	Thr	Ile	Asn	Tyr	Arg	Thr	Asn	Ile
Gly	Phe	Pro	Ala	150	Ala	Pro	Gln	Leu	Pro	Ile	Thr	Gln	Arg	Asn	Leu
Phe	Leu	Asp	Gln	165	Arg	Phe	Ala	Leu	Asp	Trp	Val	Gln	Arg	Asn	Ile
Ala	Phe	Gly	Gly	180	Asp	Pro	Arg	Lys	Val	Thr	Ile	Phe	Gly	Gln	Ser
Gly	Gly	Arg	Ser	200	Val	Asp	Val	Leu	Leu	Thr	Ser	Met	Pro	His	Asn
Pro	Phe	Arg	Ala	215	Ala	Ile	Met	Glu	Ser	Gly	Val	Ala	Asn	Tyr	Asn
Pro	Lys	Gly	Asp	230	Leu	Ser	Glu	Pro	Trp	Asn	Thr	Thr	Val	Gln	Ala
Asn	Cys	Thr	Thr	245	Ser	Ile	Asp	Ile	Leu	Ser	Cys	Met	Arg	Arg	Val
Leu	Ala	Thr	Leu	260	Met	Asn	Thr	Ile	Glu	Gln	Leu	Gly	Leu	Gly	Phe
Tyr	Thr	Leu	Asp	275	Asn	Val	Thr	Ala	Val	Tyr	Arg	Ser	Glu	Thr	Ala
Thr	Thr	Gly	Asp	290	Ile	Ala	Arg	Val	Pro	Val	Leu	Val	Gly	Thr	Val
Asn	Asp	Gly	Leu	305	Leu	Phe	Val	Leu	Gly	Glu	Asn	Asp	Thr	Gln	Ala
Leu	Glu	Glu	Ala	320	Ile	Pro	Asn	Gln	Pro	Asp	Leu	Tyr	Gln	Thr	Leu
Gly	Ala	Tyr	Pro	335	Ile	Gly	Ser	Pro	Gly	Ile	Gly	Ser	Pro	Gln	Asp
Ile	Ala	Ala	Ile	350	Glu	Thr	Glu	Val	Arg	Phe	Gln	Cys	Pro	Ser	Ala
Val	Ala	Gln	Asp	365	Ser	Arg	Asn	Arg	Gly	Ile	Pro	Ser	Trp	Arg	Tyr
Tyr	Asn	Ala	Thr	380	Phe	Glu	Asn	Leu	Glu	Leu	Phe	Pro	Gly	Ser	Glu
Tyr	His	Ser	Ser	395	Glu	Val	Gly	Met	Val	Phe	Gly	Thr	Tyr	Pro	Val
Ser	Ala	Thr	Ala	410	Leu	Glu	Ala	Gln	Thr	Ser	Lys	Tyr	Met	Gln	Gly
Trp	Ala	Ala	Phe	425	Ala	Lys	Asn	Pro	Met	Asn	Gly	Pro	Gly	Trp	Lys
Val	Pro	Asn	Val	440	Ala	Ala	Leu	Gly	Ser	Pro	Gly	Lys	Ala	Ile	Gln
Asp	Val	Ser	Pro	455	Ala	Thr	Ile	Asp	Gln	Arg	Cys	Ala	Leu	Tyr	Thr
Tyr	Tyr	Thr	Glu	470	Leu	Gly	Thr	Ile	Ala	Pro	Arg	Thr	Phe	Gly	Gly
Ser	Gly	Gly	Gly	485	Ser	Gly	Gly	Gly	Ser	Lys	Asp	Asn	Val	Ala	Asp
Val	Val	Val	Gly	500	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys
Gln	Ala	Ala	Gly	515	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg


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<223> Barley alpha amylase signal sequence: BEST1
       mature: artificial spacer: and K:trAPAO. For
       plant expression.

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<223> Barley alpha amylase signal sequence.

<221> mat_peptide
<222> (73)...(1545)
<223> BEST1 mature

<221> misc_feature
<222> (1546)...(1584)
<223> Artificial spacer sequence

<221> misc_feature
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<223> K:trAPAO

<221> CDS
<222> (1)...(2973)

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<222> (1585)...(1587)
<223> Extra lysine

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          -20                      -15                      -10

ctc tcc gcc tcc ctc gcc agc ggc acg gat ttt ccg gtc cgc agg acc      96
Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr
          -5                      1                      5

gat ctg ggc cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt cgc      144
Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg
          10                      15                      20

gga ata ccc tat gca gcg ccg ccg gtg ggc ggg ctg cgt tgg aag ccg      192
Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro
          25                      30                      35                      40

ccc caa cac gcc cgg ccc tgg gcg ggc gtt cgc ccc gcc acc caa ttt      240
Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe
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ggc tcc gac tgc ttc ggc gcg gcc tat ctt cgc aaa ggc agc ctc gcc      288
Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala
          60                      65                      70

ccc ggc gtg agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca      336
Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser
          75                      80                      85

ggc gct aaa ccc ggc cag tac ccc gtc atg gtc tgg gtc tac ggc ggc      384
Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly
          90                      95                      100

ggc ttc gcc ggc ggc acg gcc gcc atg ccc tac tac gac ggc gag gcg      432
Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala

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105		110		115		120	
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Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn							
		125		130		135	
atc ctg ggc ttt ttc gcc cat cct ggt ctc tcg cgc gag agc ccc acc							528
Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr							
		140		145		150	
gga act tcg ggc aac tac ggc cta ctc gac att ctc gcc gct ctt cgg							576
Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg							
		155		160		165	
tgg gtg cag agc aac gcc cgc gcc ttc gga ggg gac ccc ggc cga gtg							624
Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val							
		170		175		180	
acg gtc ttt ggt gaa tcg gcc gga gcg agc gcg atc gga ctt ctg ctc							672
Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu							
		185		190		195	200
acc tcg ccg ctg agc aag ggt ctc ttc cgt ggc gct atc ctc gaa agt							720
Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser							
		205		210		215	
cca ggg ctg acg cga ccg ctc gcg acg ctc gcc gac agc gcc gcc tcg							768
Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser							
		220		225		230	
ggc gag cgc ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac cca							816
Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro							
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gcc acc ctg atg gcg cgc gcc gac gcg gcc cgc ccg gca tcg cgg gac							864
Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp							
		250		255		260	
ctg cgc agg ccg cgt ccg acc gga ccg atc gtc gat ggc cat gtg ctg							912
Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu							
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ccg cag acc gac agc gcg gcg atc gcg gcg ggg cag ctg gcg ccg gtt							960
Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val							
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ccg gtc ctg atc gga acc aat gcc gac gaa ggc cgc gcc ttc ctc ggg							1008
Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly							
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cgc gcg ccg atg gag acg cca gcg gac tac caa gcc tat ctg gag gcg							1056
Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala							
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cag ttt ggc gac caa gcc gcc gcc gtg gcg gcg tgc tat ccc ctc gac							1104
Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp							
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ggc cgg gcc acg ccc aag gaa atg gtc gcg cgc atc ttc ggc gac aat							1152
Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn							
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cag ttc aat cgg ggg gtc tcg gcc ttc tcg gaa gcg ctt gtg cgc cag	1200
Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln	
365 370 375	
ggc gcg ccc gtg tgg cgt tat cag ttc aac ggt aat acc gag ggt gga	1248
Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly	
380 385 390	
aga gcg ccg gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg	1296
Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val	
395 400 405	
ttc aag ctc gac gag ttg ggt ctg ttc gat tgg ccg ccc gag ggg ccc	1344
Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro	
410 415 420	
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Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val	
425 430 435 440	
cgg ttc gcc aag aat ggc gac ccc gcc ggg gac gcc ctt acc tgg cct	1440
Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro	
445 450 455	
gcc tat tct acg ggc aag tcg acc atg aca ttc ggt ccc gag ggc cgc	1488
Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg	
460 465 470	
gcg gcg gtg gtg tcg ccc gga cct tcc atc ccc cct tgc gcg gat ggc	1536
Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly	
475 480 485	
gcc aag gcg ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc	1584
Ala Lys Ala Gly Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser	
490 495 500	
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt	1632
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly	
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ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt	1680
Leu Glu Thr Ala Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val	
525 530 535	
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg	1728
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser	
540 545 550	
ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat	1776
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn	
555 560 565	
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Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu	
570 575 580	
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa	1872
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	
585 590 595 600	
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag	1920
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	

605					610					615					
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atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag	Ile Glu Glu His 635	Leu Gln Asp 640	Lys Ala Ser Pro 645	Gln Ala Lys	2016										
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac	Arg Leu Asp Ser Val Ser 650	Phe Ala His Tyr Cys 655	Glu Lys Glu Leu 660	Asn	2064										
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc	Leu Pro Ala Val Leu 665	Gly Val Ala Asn Gln 670	Ile Thr Arg Ala Leu 675	Leu Leu 680	2112										
ggg gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	Gly Val Glu Ala His 685	Glu Ile Ser Met Leu 690	Phe Leu Thr Asp Tyr Ile 695		2160										
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc	Lys Ser Ala Thr Gly Leu 700	Asn Ile Phe Ser Asp Lys 705	Lys Lys Asp Gly 710		2208										
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc	Gly Gln Tyr Met Arg Cys 715	Lys Thr Gly Met Gln Ser 720	Ile Cys His Ala 725		2256										
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc	Met Ser Lys Glu Leu Val 730	Pro Gly Ser Val His Leu 735	Asn Thr Pro Val 740		2304										
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg	Ala Glu Ile Glu Gln 745	Ala Ser Gly Cys Thr Val Arg Ser Ala Ser 750			2352										
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gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc	Val Trp Asp Lys Pro Trp 810	Trp Arg Glu Gln Gly Phe Ser Gly Val Leu 815			2544										
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac	Gln Ser Ser Cys Asp 825	Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp 830			2592										
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga	Val Asp Arg Gln Trp 845	Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly 850			2640										

[illegible]

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Asp	Leu	Gly	Gln	Val	Gln	Gly	Leu	Ala	Gly	Asp	Val	Met	Ser	Phe	Arg	
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Gly	Ile	Pro	Tyr	Ala	Ala	Pro	Pro	Val	Gly	Gly	Leu	Arg	Trp	Lys	Pro	
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Pro	Gln	His	Ala	Arg	Pro	Trp	Ala	Gly	Val	Arg	Pro	Ala	Thr	Gln	Phe	
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Gly	Ser	Asp	Cys	Phe	Gly	Ala	Ala	Tyr	Leu	Arg	Lys	Gly	Ser	Leu	Ala	
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Pro	Gly	Val	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	Trp	Ala	Pro	Ser	
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Gly	Ala	Lys	Pro	Gly	Gln	Tyr	Pro	Val	Met	Val	Trp	Val	Tyr	Gly	Gly	
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Ile	Leu	Gly	Phe	Ala	His	Pro	Gly	Leu	Ser	Arg	Glu	Ser	Pro	Thr		
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Thr	Val	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ser	Ala	Ile	Gly	Leu	Leu	Leu
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Thr	Ser	Pro	Leu	Ser	Lys	Gly	Leu	Phe	Arg	Gly	Ala	Ile	Leu	Glu	Ser
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Pro	Gly	Leu	Thr	Arg	Pro	Leu	Ala	Thr	Leu	Ala	Asp	Ser	Ala	Ala	Ser
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Thr	Pro	Ala	Asp	Arg	Ala	Leu	Gly	Gln	Leu	Met	Ser	Ser	Ala	Trp	Val
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Ala	Tyr	Ser	Thr	Gly	Lys	Ser	Thr	Met	Thr	Phe	Gly	Pro	Glu	Gly	Arg
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Ala	Ala	Val	Val	Ser	Pro	Gly	Pro	Ser	Ile	Pro	Pro	Cys	Ala	Asp	Gly
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Ala	Lys	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser
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Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly
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Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val
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Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu
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Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	
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Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	
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Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	
745					750					755					760	
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	
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Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	
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Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	
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Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	
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 2227-3615, K:trAPAO, extra lysine; 3616-3618, stop
 codon. For bacterial expression.

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act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg      96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
          20          25          30

tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg      144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
          35          40          45

ggg ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa      192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
          50          55          60

tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac      240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
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atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa      288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
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gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt      336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
          100          105          110

aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa      384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
          115          120          125

atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat      432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
          130          135          140

ggg gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat      480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
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gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta      528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
          165          170          175

gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac      576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
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Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
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Gly Ser Pro Glu Phe Ala Pro Thr Val Lys Ile Asp Ala Gly Met Val	
225 230 235 240	
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Val Gly Thr Thr Thr Val Pro Gly Thr Thr Ala Thr Val Ser Glu	
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Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe Ala Pro Pro	
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Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr Ala Tyr Gly	
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Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu Arg Glu Ile	
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Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu Asn Thr Asn	
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Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu Tyr Gly Trp	
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Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu Gly Phe Pro	
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Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly Phe Leu Asp	
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Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala Ala Phe Gly	
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Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala Gly Gly Arg	
420 425 430	
agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca ccc ttc cga	1344
Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro Pro Phe Arg	

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acc agt atc gac atc ttg agt tgt atg aga aga gtc gat ctc gcc act Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp Leu Ala Thr 485 490 495			1488
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acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg tac cac agc Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val Tyr His Ser 625 630 635 640			1920
tct gaa gtc ggg atg gtg ttt ggc acg tat cct gtc gca agt gcg acc Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala Ser Ala Thr 645 650 655			1968
gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc tgg gcg gcc Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala Trp Ala Ala 660 665 670			2016
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Ala Leu Glu Ala Gln	Thr Ser Lys Tyr Met	Gln Gly Ala Trp Ala Ala
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Glu Leu Gly Thr Ile	Ala Pro Arg Thr Phe	Gly Gly Gly Ser Gly Gly
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Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu
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His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr
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 polylinker, 688-2163, BEST1 mature; 2164-2199,
 spacer, 2200-3588, K:trAPAO

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act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg      96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
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tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg      144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
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ggg ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa      192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
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Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
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Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
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gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt      336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
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aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa      384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
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Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
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ggg gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat      480
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Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
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Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
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Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
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Gly Ser Pro Glu Phe Thr Asp Phe Pro Val Arg Arg Thr Asp Leu Gly	
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Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg Gly Ile Pro	
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Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro Pro Gln His	
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Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe Gly Ser Asp	
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Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala Pro Gly Val	
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Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser Gly Ala Lys	
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Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly Gly Phe Ala	
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Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala Leu Ala Arg	
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Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val Thr Val Phe	
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Leu	Ser	Lys	Gly	Leu	Phe	Arg	Gly	Ala	Ile	Leu	Glu	Ser	Pro	Gly	Leu		
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Thr	Arg	Pro	Leu	Ala	Thr	Leu	Ala	Asp	Ser	Ala	Ala	Ser	Gly	Glu	Arg		
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Pro	Arg	Pro	Thr	Gly	Pro	Ile	Val	Asp	Gly	His	Val	Leu	Pro	Gln	Thr		
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Ile	Gly	Thr	Asn	Ala	Asp	Glu	Gly	Arg	Ala	Phe	Leu	Gly	Arg	Ala	Pro		
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Asp	Glu	Leu	Gly	Leu	Phe	Asp	Trp	Pro	Pro	Glu	Gly	Pro	Thr	Pro	Ala		
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gac	cgt	gcg	ctg	ggc	caa	ctg	atg	tcc	tcc	gcc	tgg	gtc	cgg	ttc	gcc	2016	
Asp	Arg	Ala	Leu	Gly	Gln	Leu	Met	Ser	Ser	Ala	Trp	Val	Arg	Phe	Ala		
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Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly Ala Lys Ala	
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Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu	
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acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca	2544
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His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp	
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Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala	
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Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu	
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Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg		
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Thr	Pro	Lys	Glu	Met	Val	Ala	Arg	Ile	Phe	Gly	Asp	Asn	Gln	Phe	Asn	
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Lys	Asn	Gly	Asp	Pro	Ala	Gly	Asp	Ala	Leu	Thr	Trp	Pro	Ala	Tyr	Ser	
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Thr	Gly	Lys	Ser	Thr	Met	Thr	Phe	Gly	Pro							

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His Ser Leu Gln Asp	Leu Lys Ala Ser Pro	Gln Ala Lys Arg	Leu Asp	
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Ser Val Ser Phe	Ala His Tyr Cys Glu Lys	Glu Leu Asn Leu	Pro Ala	
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Val Leu Gly Val	Ala Asn Gln Ile Thr	Arg Ala Leu Leu	Gly Val Glu	
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Ala His Glu Ile	Ser Met Leu Phe	Leu Thr Asp Tyr	Ile Lys Ser Ala	
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Thr Gly Leu Ser	Asn Ile Phe Ser	Asp Lys Lys Asp	Gly Gly Gln Tyr	
	930	935	940	
Met Arg Cys Lys	Thr Gly Met Gln Ser	Ile Cys His Ala	Met Ser Lys	
945	950	955	960	
Glu Leu Val Pro	Gly Ser Val His Leu	Asn Thr Pro Val	Ala Glu Ile	
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Glu Gln Ser Ala	Ser Gly Cys Thr Val	Arg Ser Ala Ser	Gly Ala Val	
	980	985	990	
Phe Arg Ser Lys	Lys Val Val Val	Ser Leu Pro Thr	Thr Leu Tyr Pro	
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Thr Leu Thr Phe	Ser Pro Pro Leu	Pro Ala Glu Lys	Gln Ala Leu Ala	
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Glu Asn Ser Ile	Leu Gly Tyr Tyr Ser	Lys Ile Val Phe	Val Trp Asp	
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Lys Pro Trp Trp	Arg Glu Gln Gly Phe	Ser Gly Val Leu	Gln Ser Ser	
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Cys Asp Pro Ile	Ser Phe Ala Arg	Asp Thr Ser Ile	Asp Val Asp Arg	
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Gln Trp Ser Ile	Thr Cys Phe Met	Val Gly Asp Pro	Gly Arg Lys Trp	
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Ser Gln Gln Ser	Lys Gln Val Arg	Gln Lys Ser Val	Trp Asp Gln Leu	
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Arg Ala Ala Tyr	Glu Asn Ala Gly	Ala Gln Val Pro	Glu Pro Ala Asn	
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Val Leu Glu Ile	Glu Trp Ser Lys	Gln Gln Tyr Phe	Gln Gly Ala Pro	
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Ser Ala Val Tyr	Gly Leu Asn Asp	Leu Ile Thr Leu	Gly Ser Ala Leu	
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Arg Thr Pro Phe	Lys Ser Val His	Phe Val Gly Thr	Glu Thr Ser Leu	
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Val Trp Lys Gly	Tyr Met Glu Gly	Ala Ile Arg Ser	Gly Gln Arg Gly	
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 and linker, nt 1-687; Glyc (-) APAO, nt 688-2490;
 mutation in putative glycosylation sites in bold
 and underlined, nt 1288-1290 (AAT->TCC) and nt
 1303-1305 (AGC->AAC).

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 <222> (1)...(687)
 <223> GST and linker

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<223> Glyc (-) APAO

<221> mutation
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act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg      96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
          20          25          30

tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg      144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
          35          40          45

ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa      192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
          50          55          60

tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac      240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
          65          70          75          80

atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa      288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
          85          90          95

gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt      336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
          100          105          110

aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa      384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
          115          120          125

atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat      432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
          130          135          140

ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat      480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
          145          150          155          160

gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta      528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
          165          170          175

gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac      576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
          180          185          190

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Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
210 215 220	
gga tcc ccg gaa ttc atg gca ctt gca ccg agc tac atc aat ccc cca	720
Gly Ser Pro Glu Phe Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro	
225 230 235 240	
aac gtc gcc tcc cca gca ggg tat tct cac gtc ggc gta ggc cca gac	768
Asn Val Ala Ser Pro Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp	
245 250 255	
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Gly Gly Arg Tyr Val Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser	
260 265 270	
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Gly Val Thr Asp Pro Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala	
275 280 285	
aat ctg cga gct tgc ctt gct gca gtt gga gcc act tca aac gac gtc	912
Asn Leu Arg Ala Cys Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val	
290 295 300	
acc aag ctc aat tac tac atc gtc gac tac gcc ccg agc aaa ctc acc	960
Thr Lys Leu Asn Tyr Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr	
305 310 315 320	
gca att gga gat ggg ctg aag gct acc ttt gcc ctt gac agg ctc cct	1008
Ala Ile Gly Asp Gly Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro	
325 330 335	
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Pro Cys Thr Leu Val Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu	
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Phe Glu Val Asp Ala Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp	
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Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu	
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Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu	
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Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro	
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Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Ser Asp Ser	
420 425 430	
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Asn Gln Asn Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly	

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Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	
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Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	
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Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	
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Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	
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Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	
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Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	
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Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	
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Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	
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Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	
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cga	caa	tgg	tcc	att	acc	tgt	ttc	atg	gtc	gga	gac	ccg	gga	cgg	aag	2160
Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	
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Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	
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Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	
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Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	
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ccg	agc	gcc	gtc	tat	ggg	ctg	aac	gat	ctc	atc	aca	ctg	ggg	tcg	gcg	2352
Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	
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Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	
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Thr	Lys	Leu	Asn	Tyr	Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys
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Phe	Glu	Val	Asp	Ala	Thr	Ala	Leu	Val	Pro	Gly	His	Thr	Thr
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													Leu

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		755					760					765					
Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala		
	770					775					780						
Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser		
785					790					795					800		
Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg		
				805					810						815		
Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala					
			820					825									